WHAT IS CLAIMED IS:

1. A method comprising:

performing a plurality of fermentations, each fermentation in a different sample vessel; and

performing a further processing step on the plurality of fermented samples where the sample is retained in the same sample vessel as the fermentation during the processing step.

2. The method of claim 1, wherein the further processing step is centrifugation of the fermented samples in the sample vessels in which the fermentations were performed.

3. The method of claim 1, wherein performing a plurality of fermentations includes attaching a fermentor head to the plurality of sample vessels.

4. The method of claim 1, further comprising grasping the sample vessels with a robotic gripper apparatus in order to move the sample vessels from a first location where the fermentations are performed to a second location where the further processing step is performed.

5. The method of claim 1, wherein the fermentations comprise fermentations of prokaryotic or eukaryotic cells, or viral particles.

6. The method of claim 1, wherein the fermentation is an aerobic fermentation.

7. The method of claim 1, wherein the fermentation is an anaerobic fermentation.

8. The method of claim 1, wherein the further processing step comprises aspirating the sample.

9. The method of claim 1, wherein the further processing step comprises sonicating the sample.

10. The method of claim 1, wherein the further processing step comprises washing the sample.

11. The method of claim 1, wherein the further processing step comprises agitating the sample.

12. The method of claim 1, wherein the fermentation is a bacterial fermentation where a recombinant protein is expressed.

13. The method of claim 1 wherein the further processing step comprises lysing cells in the fermented samples.

14. The method of claim 1, wherein the method further comprises isolating recombinant proteins expressed during the fermentations after the further processing step.

15. The method of claim 14, wherein the recombinant proteins are isolated by column chromotography.

16. The method of claim 14, wherein the method further comprises crystallizing the isolated recombinant proteins.

17. The method of claim 16, wherein the method includes crystallizing tens to thousands of proteins per day.

18. The method of claim 16, wherein the crystallized proteins are used to design drug.

19. The method of claim 16, wherein a structure of the crystallized proteins are analyzed by x-ray crystallography.

20. The method of claim 19, wherein the protein structures are used in computer assisted drug design.

21. The method of claim 1, wherein the method uses a robot that tests tens to thousands of variants of a protein.

22. The method of claim 21, wherein the robot includes a plate handler that carries plates from one station to another.

23. The method of claim 1, wherein the samples comprise a prokaryotic, eukaryotic, or viral expression system comprising a gene fragment or variant in a vector.

24. The method of claim 1, wherein performing a plurality of fermentations includes performing at least 96 fermentations at the same time.

25. The method of claim 1, wherein hundreds of fermentations are performed per day using the method.

26. The method of claim 16, further comprising analyzing on an imaging station more than 1 million images from thousands of the crystallizations.

27. The method of claim 16, further comprising identifying crystals from the crystallizations using crystal detecting algorithms.

28. The method of claim 16, further comprising using a robot to mount and center about 30 to about 50 crystals per hour with a robot.

29. The method of claim 28, wherein the crystals are frozen and then analyzed by X-ray diffraction.

30. The method of claim 29, wherein the diffraction data is subject to phasing and refinement calculations and is converted to a three dimensional representation of the protein.

31. The method of claim 30, wherein the three dimensional representation of the protein undergoes virtual ligand screening wherein a computerized simulation of the interaction between proteins and potential drugs identifies drug leads for synthesis and/or in vitro and/or in vivo testing.

32. A system form processing a plurality of samples comprising:

a first station for performing a plurality of fermentations, each fermentation being performed in a different sample vessel; and

a second station for performing a further processing step on the plurality of fermented samples where the sample is retained in the same sample vessel as the fermentation during the further processing step.

33. The system of claim 32, wherein the second station comprises an centrifuge system.

34. The system of claim 32, wherein the first station further comprises a process controller.

35. The system of claim 32, further comprising a robotic gripper apparatus for moving the samples from the first station to the second station.

36. The system of claim 32, wherein the first station is adapted to ferment bacteria or eukaryotic cells.

37. The system of claim 32, wherein the first station is adapted to perform aerobic fermentations.

38. The system of claim 32, wherein the first station is adapted to perform anaerobic fermentations.

39. The system of claim 32, further comprising means for aspirating the samples.

40. The system of claim 32, further comprising means for sonicating the samples.

41. The system of claim 32, further comprising means for washing the samples.

42. The system of claim 32, further comprising means for agitating the samples.

43. The system of claim 32, further comprising means for lysing the samples.

44. The system of claim 32, further comprising means for pipetting the samples.

45. The system of claim 42, further comprising means for purifying proteins expressed in the samples.

46. The system of claim 32, further comprising means for crystallizing proteins expressed in the samples.

47. The system of claim 46, wherein the means is capable of crystallizing hundreds of thousands proteins per day.

48. The system of claim 32, wherein the system further comprises a robot that tests thousands of variants of a protein.

49. The system of claim 48, wherein the robot includes a plate handler that carries plates from one station to another.

50. The system of claim 32, wherein the system further comprises means for performing x-ray crystallography.

51. The system of claim 32, wherein the fermentation simultaneously ferments 96 samples at a time.

52. The system of claim 32, wherein the first station is capable of performing hundreds of fermentations per day.

53. The system of claim 32, further comprising means for analyzing on an imaging station as many as 1 million images from as many as 140,000 crystallization experiments set up each day.

54. The system of claim 32, further comprising means for identifying crystals with crystal detecting algorithms.

55. The system of claim 32, further comprising means for automatically positioning and centering about 30 to about 50 protein crystals per hour with a robot.

56. The system of claim 48, wherein the crystals are frozen and analyzed with by X-ray diffraction.

57. The system of claim 56, wherein the beamline produces diffraction data that is subject to phasing and refinement calculations and is converted to a three dimensional representation of the protein.

58. The system of claim 57, wherein the three dimensional representation of the protein undergoes virtual ligand screening wherein a computerized simulation of the interaction between proteins and potential drugs identifies drug leads for synthesis and/or in vitro and/or in vivo testing.